

INTERNATIONAL SEARCH REPORT

Inte: Application No
PCT/US 00/25856

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/54 C12N9/10 C12N15/82 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, STRAND, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Database, Heidelberg, FRG Empln accession number AB023482 15 March 1999 SASAKI, T. ET AL.: "Oryza sativa genomic DNA, chromosome 6, clone P0680A03" XP002167058	1,3,4
Y	the whole document	2
X	EMBL Database, Heidelberg, FRG Empln accession number AB020755 14 December 1998 NAKAMURA, Y.: "Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1" XP002160876	1,3
Y	the whole document	2,4

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

10 May 2001

Date of mailing of the international search report

28.05.01

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INTERNATIONAL SEARCH REPORT

Inte Application No
PCT/US 00/25856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Database, Heidelberg, FRG Empln accession number AB011483 10 March 1998 NAKAMURA, Y.: "Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9" XP002160878 cited in the application	1,3
Y	the whole document ---	2,4
X	EMBL Database, Heidelberg, FRG Empln accession number AC007584 19 May 1999 LIN, X. ET AL.: "Arabidopsis thaliana chromosome II section 101 of 255 of the complete sequence. Sequence from clones MJB20, T19E12" XP002167059	1,3
Y	the whole document ---	2,4
X	EMBL Database, Heidelberg, FRG Emest_Pln2 accession number AI965398 24 August 1999 SHOEMAKER, R. ET AL.: "sc71b10.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-1844 5' similar to SW: Y506_SYNY3 Q55482 HYPOTHETICAL 28.8 KD PROTEIN SLL0506, mRNA sequence" XP002167060	1,3
Y	the whole document ---	2,4
X	EMBL Database, Heidelberg, FRG Emest_Pln2 accession number AU069089 07 June 1999 SASAKI, T.: "Oryza sativa cDNA, partial sequence (C52041_1A)" XP002160877	1
A	the whole document ---	13-15
X	EMBL Database, Heidelberg, FRG Emest_Pln4 accession number AW038635 17 September 1999 D'ASCENZO, M. ET AL.: "EST280318 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET7I9, mRNA sequence" XP002167061	1
A	the whole document ---	13-15
	-/--	

INTERNATIONAL SEARCH REPORT

Intel. of Application No.

PCT/US 00/25856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	APFEL, C.M. ET AL.: "Use of Genomics To Identify Bacterial Undecaprenyl Pyrophosphate Synthetase" JOURNAL OF BACTERIOLOGY, vol. 181, no. 2, January 1999 (1999-01), pages 483-492, XP002160874 cited in the application	2,4
A	abstract page 486 -page 487; figure 3 page 488, column 1, line 7 -column 2, line 3 page 490, column 2, line 36 - line 64	1,3,5-15
A	SHIMIZU, N. ET AL.: "Molecular Cloning, Expression, and Purification of Undecaprenyl Diphosphate Synthase" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 31, 31 July 1998 (1998-07-31), pages 19476-19481, XP002160875 cited in the application the whole document	1-15
A	DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; PHYTOCHEMICAL ANALYSIS, vol. 8, no. 3, 1997 CORNISH, K. & BARTLETT, D.L.: "Stabilisation of particle integrity and particle bound cis-prenyl transferase activity in stored, purified rubber particles" XP002161336 abstract	1-15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/25856

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-15 partially

An isolated nucleic acid fragment encoding a plant cis-prenyltransferase polypeptide selected from the group consisting of a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence SEQ ID NO: 2, b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of SEQ ID NO: 2, c) an isolated nucleic acid fragment derived from *Dimorphotheca* encoding a polypeptide having at least 41% identity with the amino acid sequence SEQ ID NO: 24, d) an isolated nucleic acid fragment derived from *Dimorphotheca* having at least 50% identity with the nucleic acid sequence SEQ ID NO: 23, e) an isolated nucleic acid fragment that hybridizes with said nucleic acid sequences, f) an isolated nucleic acid fragment that hybridizes with the nucleic acid sequence SEQ ID NO: 1, g) an isolated nucleic acid fragment that is complementary to said nucleic acid sequences, said isolated nucleic acid fragment having the nucleic acid sequence SEQ ID NO: 1, a polypeptide encoded by said isolated nucleic acid fragment, said polypeptide having the amino acid sequence SEQ ID NO: 2, a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence of a plant cis-prenyltransferase polypeptide comprising a hybridization step involving said nucleic acid fragment, a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence of a plant cis-prenyltransferase polypeptide comprising a cDNA amplification step involving primers corresponding to a portion of SEQ ID NO: 1, a chimeric gene comprising said nucleic acid fragment, a transformed host cell comprising said chimeric gene and a method of altering the level of expression of a plant cis-prenyltransferase polypeptide in a host cell;

2. Claims: 1-15 partially

Idem as subject 1 but limited to *Calendula officinalis* and SEQ ID NOS: 3 and 4;

3. Claims: 1-15 partially

Idem as subject 1 but limited to *Hevea brasiliensis* and SEQ ID NOS: 5-10;

4. Claims: 1-15 partially

Idem as subject 1 but limited to *Vitis* sp. and SEQ ID NOS:

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

11 and 12;

5. Claims: 1-15 partially

Idem as subject 1 but limited to *Oryza sativa* and SEQ ID NOS: 13-16;

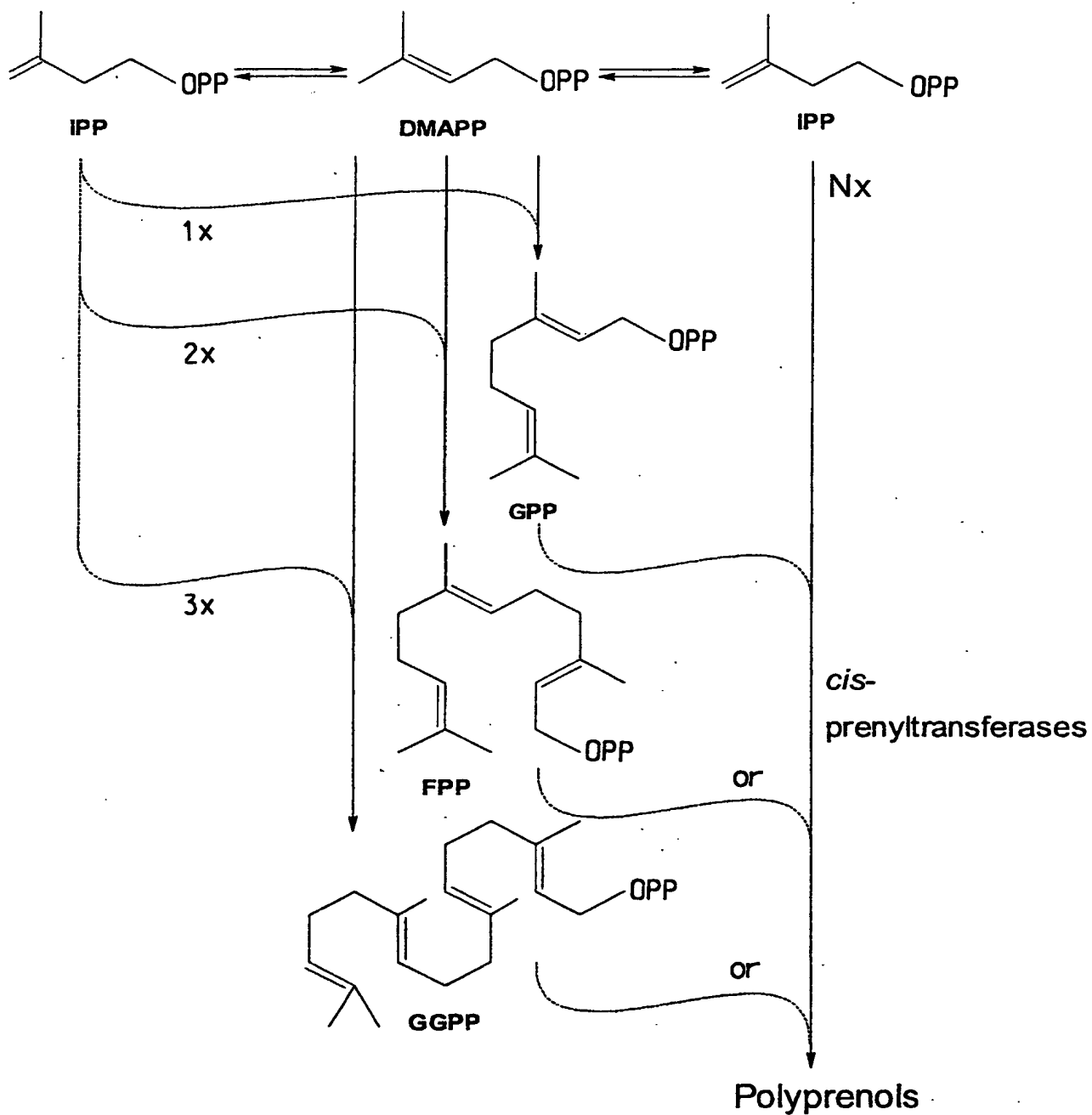
6. Claims: 1-15 partially

Idem as subject 1 but limited to *Glycine max* and SEQ ID NOS: 17 and 18;

7. Claims: 1-15 partially

Idem as subject 1 but limited to *Triticum aestivum* and SEQ ID NOS: 19 and 20.

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Polyprenol biosynthesis**FIG. 1**

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FIG. 2-3

sll.pk0128.h7	(SEQ ID NO:17)	(199)	GATACGGAGTCTCGCTGCGCCCAAGCTGCTGTGAGCCACAT---CCGGC
vdb1c.pk001.k23	(SEQ ID NO:11)	(169)	GAGGAAGAAGCAAGAGAAGAAACAGAGAGCGGCTGATAT---CCGGC
wdk5c.pk005.f22	(SEQ ID NO:19)	(30)	GCGG---GCCGTACCGCTCCGCGCGCGCGCTCCGCTCC---TCAC
M.lutupps	(SEQ ID NO:23)	(1)	-----ATGTTTCCAATTAGAGCGGAAAGCAATAAAAAT
yeast rer2	(SEQ ID NO:25)	(21)	ACCTGGTCATTCATTTGTAAAGTGGACAAACATCTTTTCGGCA
yeast srl1	(SEQ ID NO:27)	(128)	TAGCTTGTTTTCATGG-TTATATATAATCTTCAGATATTTTGATAA
dms2c.pk005.c7	(SEQ ID NO:1)	251	AGGAG-CAAGCACAGTTATCCCAAGATGCGAGTGAATGATGGA
ecs1c.pk009.p19	(SEQ ID NO:3)	(150)	-----TCCCAAGACCTTGGATGATATATGGA
ehb2c.pk001.i10	(SEQ ID NO:5)	(74)	GCATCCAAACCCACGTCCCTCCCTCTCATATGCTTCTGATATGGA
ehb2c.pk001.d17	(SEQ ID NO:7)	(74)	GCATCCAAACCCACGTCCCTCCCTCTCATATGCTTCTGATATGGA
ehb2c.pk001.o18	(SEQ ID NO:9)	(74)	GCATCCAAACCCACGTCCCTCCCTCTCATATGCTTCTGATATGGA
r10n.pk117.i23	(SEQ ID NO:13)	(1)	-----TCCCAAGACCTTGGATGATATATGGA
rr1.pk005.h8	(SEQ ID NO:15)	(122)	CTGTCTCTCGTATGCGCAATCCCTTCAATATGGAATATATGGA
sll.pk0128.h7	(SEQ ID NO:17)	(246)	GGAAG-TCGCGCGAGAGATGTCCTCGAGATGCTGCGGTGATATGGA
vdb1c.pk001.k23	(SEQ ID NO:11)	(216)	CGGTG-ATCGGAGAGAAATGATCCCGGAACTGCGGTGATATGGA
wdk5c.pk005.f22	(SEQ ID NO:19)	(72)	AGGGG-TCGCGCGAGTCTGCTCCGCGGATCTGCGGTGATATGGA
M.lutupps	(SEQ ID NO:23)	(38)	ATAAATAATGCGCAAAATTCGGAACTATATGGAATGATATGGA
yeast rer2	(SEQ ID NO:25)	(71)	CATTGCGTGCATCTAACTGTGACCTAGCAATGCGGTGATATGGA
yeast srl1	(SEQ ID NO:27)	(177)	AGCAT-TAAGGGTATGGGACAGTCCCTGAACTCTCTTATATGGA
dms2c.pk005.c7	(SEQ ID NO:1)	301	CGAAGACGATCGGTGATCAGTCGTAAATGCCGATGCTGGTAT
ecs1c.pk009.p19	(SEQ ID NO:3)	(31)	CGAAGCCTCTCGTTCGCGGTGAAACCTGCTGCTCCATGACCGGGA
ehb2c.pk001.i10	(SEQ ID NO:5)	(124)	CGAAGACGATCGTTCGTAAGACCTTAACTGCGAAGAGGTGGTGA
ehb2c.pk001.d17	(SEQ ID NO:7)	(124)	CGAAGACGATCGTTCGTAAGACCTTAACTGCGAAGAGGTGGTGA
ehb2c.pk001.o18	(SEQ ID NO:9)	(124)	CGAAGACGATCGTTCGTAAGACCTTAACTGCGAAGAGGTGGTGA
r10n.pk117.i23	(SEQ ID NO:13)	(31)	CGTAACCTCTCGTTCGTAAGACCTTAACTGCGAAGAGGTGGTGA
rr1.pk005.h8	(SEQ ID NO:15)	(172)	CGTAACCTCTCGTTCGTAAGACCTTAACTGCGAAGAGGTGGTGA
sll.pk0128.h7	(SEQ ID NO:17)	(295)	GGGAAGGGAAGTGGCGGAGTGAAGGCTTCCGACCTCCGCGGGA
vdb1c.pk001.k23	(SEQ ID NO:11)	(265)	GGGAAGGGAAGTGGCGGAGTGAAGGCTTCCGACCTCCGCGGGA
wdk5c.pk005.f22	(SEQ ID NO:19)	(121)	GGGAAGTCCGCTGGCGGAGCGCGGCTTCCGCGGCGGACGACGGGA
M.lutupps	(SEQ ID NO:23)	(88)	GGAAATGGCCATGGGGAACAGAAATAATGCGCGCATATAAAGGAGA
yeast rer2	(SEQ ID NO:25)	(121)	GGGAAGGGAAGTGGCGGAGTGAAGGCTTCCGACCTCCGCGGGA
yeast srl1	(SEQ ID NO:27)	(226)	GGTAACGCGAGATATGCCAAGTCAAGAGGCTTCCGATATAAAGGCGCA

ehb2c.pk001.d17 (SEQ ID NO:7)
ehb2c.pk001.o18 (SEQ ID NO:9)
r10n.pk117.i23 (SEQ ID NO:13)
 rr1.pk005.h8 (SEQ ID NO:15)
 sl1.pk0128.h7 (SEQ ID NO:17)
vdb1c.pk001.k23 (SEQ ID NO:11)
wdk5c.pk005.f22 (SEQ ID NO:19)
 M.lutups (SEQ ID NO:23)
 yeast rer2 (SEQ ID NO:25)
 yeast srl1 (SEQ ID NO:27)

dms2c.pk005.c7 (SEQ ID NO:1)
ecs1c.pk009.p19 (SEQ ID NO:3)
ehb2c.pk001.i10 (SEQ ID NO:5)
ehb2c.pk001.d17 (SEQ ID NO:7)
ehb2c.pk001.o18 (SEQ ID NO:9)
r10n.pk117.i23 (SEQ ID NO:13)
 r11.pk005.h8 (SEQ ID NO:15)
 s11.pk0128.h7 (SEQ ID NO:17)
vdb1c.pk001.k23 (SEQ ID NO:11)
wdk5c.pk005.f22 (SEQ ID NO:19)
 M.lutupps (SEQ ID NO:23)
 yeast rer2 (SEQ ID NO:25)
 yeast srl1 (SEQ ID NO:27)

dms2c.pk005.c7 (SEQ ID NO:1)
ecslc.pk009.p19 (SEQ ID NO:3)
ehb2c.pk001.i10 (SEQ ID NO:5)
ehb2c.pk001.d17 (SEQ ID NO:7)
ehb2c.pk001.o18 (SEQ ID NO:9)
r10n.pk117.i23 (SEQ ID NO:13)
rrl.pk005.h8 (SEQ ID NO:15)
s11.pk0128.h7 (SEQ ID NO:17)
vdb1c.pk001.k23 (SEQ ID NO:11)
wdk5c.pk005.f22 (SEQ ID NO:19)

FIG. 2-5

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M. lutupps	(SEQ ID NO:23)	(324)	-AAGCTGAAACGATTTGGCTTTATGTGATGATTTACCGGACCATACAA
yeast rer2	(SEQ ID NO:25)	(365)	TACCAATAAAATATCCGCGATCTCTTTGTTGGATATCTATTA
yeast srl1	(SEQ ID NO:27)	(476)	CTAAATAGAAATAGTACGGTGTCAATTTTACATCTCCAGAAAGGG
dms2c.pk005.c7	(SEQ ID NO:1)	601	CGGATCATTACATTTCTCTTAATCTCTGGAGAACCTCTACATCTCAA
ecs1c.pk009.p19	(SEQ ID NO:3)	(484)	AGTTTTCATCGAAATAGAGAAATCAAGAGCCATTTGAGAACCCA
ehb2c.pk001.i10	(SEQ ID NO:5)	(418)	ACCGAGCAGATAGGATATAGGGGTATGTCCATCTTTCCAAATGTGT
ehb2c.pk001.d17	(SEQ ID NO:7)	(418)	ACCGAGCAGATAGGATATAGGGGTATGTCCATCTTTCCAAATGTGT
ehb2c.pk001.o18	(SEQ ID NO:9)	(418)	ATCGAGCAGAAAGGATATAGGGGTATGTCCATCTTTCCAAATGTGT
r10n.pk117.i23	(SEQ ID NO:13)	(325)	GTAAGCTGAGAACTGATGGCTATCTGTGAATCAGGGACGGT
rr1.pk005.h8	(SEQ ID NO:15)	(466)	GTAAGCTGAGAACTGATGGCTATCTGTGAATCAGGGACGGT
s11.pk0128.h7	(SEQ ID NO:17)	(580)	GAATGATAGCTTGTTCAGTAAGGATTAATACAAATTTGAGATCCA
vdb1c.pk001.k23	(SEQ ID NO:11)	(547)	CTGAT---AATTGTTTACAGGAGCTTAGGAGCTCTGCGATTTACA
wdk5c.pk005.f22	(SEQ ID NO:19)	(406)	AGAGTCACGAGTCCCTAGGAGCTTACAGAACTCTGCGAGCTCGA
M. lutupps	(SEQ ID NO:23)	(373)	AAAGATGTTAGTACCGAAGAGAACTGTAACHTTTTACGTTTAAAC
yeast rer2	(SEQ ID NO:25)	(415)	GAAGATTTGGGTTCTTGTGATCTGATCTGATCTGATCTGATCTGAT
yeast srl1	(SEQ ID NO:27)	(526)	AAAAATATAAATAGTGGAAATCTACAGGTTGGAGACGATTTTAC
dms2c.pk005.c7	(SEQ ID NO:1)	651	TGTTCGTCAGCAATAAATTTATGCT--GCATAATATGATTTCTCCAGCT
ecs1c.pk009.p19	(SEQ ID NO:3)	(366)	TGTTCGTCAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACT
ehb2c.pk001.i10	(SEQ ID NO:5)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
ehb2c.pk001.d17	(SEQ ID NO:7)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
ehb2c.pk001.o18	(SEQ ID NO:9)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
r10n.pk117.i23	(SEQ ID NO:13)	(375)	-GTTTCGTCGTT-TGCATGCTTCACTCTTCTTCTTCTTCTTCTTCTTCT
rr1.pk005.h8	(SEQ ID NO:15)	(516)	-GTTTCGTCGTT-TGCATGCTTCACTCTTCTTCTTCTTCTTCTTCTTCT
s11.pk0128.h7	(SEQ ID NO:17)	(630)	AGTTTCGTCAGTGGATGATGATGATGATGATGATGATGATGATGATGAT
vdb1c.pk001.k23	(SEQ ID NO:11)	(594)	GTTCATGTCGAGCTAGCTTCACTTCACTTCACTTCACTTCACTTCACT
wdk5c.pk005.f22	(SEQ ID NO:19)	(456)	TGTAGTGTTCAGTCACTTCACTTCACTTCACTTCACTTCACTTCACT
M. lutupps	(SEQ ID NO:23)	(423)	GTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
yeast rer2	(SEQ ID NO:25)	(465)	GTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
yeast srl1	(SEQ ID NO:27)	(576)	TTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
dms2c.pk005.c7	(SEQ ID NO:1)	700	TGTTCGTCAGCAATAAATTTATGCT--GCATAATATGATTTCTCCAGCT
ecs1c.pk009.p19	(SEQ ID NO:3)	(366)	TGTTCGTCAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACT
ehb2c.pk001.i10	(SEQ ID NO:5)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
ehb2c.pk001.d17	(SEQ ID NO:7)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
ehb2c.pk001.o18	(SEQ ID NO:9)	(468)	GTTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT
r10n.pk117.i23	(SEQ ID NO:13)	(375)	-GTTTCGTCGTT-TGCATGCTTCACTCTTCTTCTTCTTCTTCTTCTTCT
rr1.pk005.h8	(SEQ ID NO:15)	(516)	-GTTTCGTCGTT-TGCATGCTTCACTCTTCTTCTTCTTCTTCTTCTTCT
s11.pk0128.h7	(SEQ ID NO:17)	(630)	AGTTTCGTCAGTGGATGATGATGATGATGATGATGATGATGATGATGAT
vdb1c.pk001.k23	(SEQ ID NO:11)	(594)	GTTCATGTCGAGCTAGCTTCACTTCACTTCACTTCACTTCACTTCACT
wdk5c.pk005.f22	(SEQ ID NO:19)	(456)	TGTAGTGTTCAGTCACTTCACTTCACTTCACTTCACTTCACTTCACT
M. lutupps	(SEQ ID NO:23)	(423)	GTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
yeast rer2	(SEQ ID NO:25)	(465)	GTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
yeast srl1	(SEQ ID NO:27)	(576)	TTTTCGTCGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT

FIG. 2-6

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FIG. 2-7

dms2c.pk005.c7	(SEQ ID NO:1)	701	TTGTCCTAAGCATGGGACTA	750
ecslc.pk009.p19	(SEQ ID NO:3)	(582)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(414)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(516)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(516)	TTGTCCTAAGCATGGGACTA	
r10n.pk117.i23	(SEQ ID NO:13)	(516)	TTGTCCTAAGCATGGGACTA	
rr1.pk005.h8	(SEQ ID NO:15)	(423)	TTGTCCTAAGCATGGGACTA	
s11.pk0128.h7	(SEQ ID NO:17)	(564)	TTGTCCTAAGCATGGGACTA	
vdbl.c.pk001.k23	(SEQ ID NO:11)	(678)	TTGTCCTAAGCATGGGACTA	
wdk5c.pk005.f22	(SEQ ID NO:19)	(642)	TTGTCCTAAGCATGGGACTA	
M.lutupps	(SEQ ID NO:23)	(504)	TTGTCCTAAGCATGGGACTA	
yeast rer2	(SEQ ID NO:25)	(471)	TTGTCCTAAGCATGGGACTA	
yeast srl1	(SEQ ID NO:27)	(513)	TTGTCCTAAGCATGGGACTA	
		(624)	TTGTCCTAAGCATGGGACTA	

dms2c.pk005.c7	(SEQ ID NO:1)	751	TTGTCCTAAGCATGGGACTA	800
ecslc.pk009.p19	(SEQ ID NO:3)	(601)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(433)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(560)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(560)	TTGTCCTAAGCATGGGACTA	
r10n.pk117.i23	(SEQ ID NO:13)	(566)	TTGTCCTAAGCATGGGACTA	
rr1.pk005.h8	(SEQ ID NO:15)	(457)	TTGTCCTAAGCATGGGACTA	
s11.pk0128.h7	(SEQ ID NO:17)	(598)	TTGTCCTAAGCATGGGACTA	
vdbl.c.pk001.k23	(SEQ ID NO:11)	(697)	TTGTCCTAAGCATGGGACTA	
wdk5c.pk005.f22	(SEQ ID NO:19)	(661)	TTGTCCTAAGCATGGGACTA	
M.lutupps	(SEQ ID NO:23)	(523)	TTGTCCTAAGCATGGGACTA	
yeast rer2	(SEQ ID NO:25)	(490)	TTGTCCTAAGCATGGGACTA	
yeast srl1	(SEQ ID NO:27)	(557)	TTGTCCTAAGCATGGGACTA	
		(674)	TTGTCCTAAGCATGGGACTA	

dms2c.pk005.c7	(SEQ ID NO:1)	801	TTGTCCTAAGCATGGGACTA	850
ecslc.pk009.p19	(SEQ ID NO:3)	(616)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(448)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(595)	TTGTCCTAAGCATGGGACTA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(595)	TTGTCCTAAGCATGGGACTA	
		(616)	TTGTCCTAAGCATGGGACTA	

FIG. 2-8

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ecs1c.pk009.p19 (SEQ ID NO:3)	(684)	TATA	-----	-----	-----
ehb2c.pk001.i10 (SEQ ID NO:5)	(842)	ACCTGGGAGATC-ATAAGGATATACTTAAATATA	-----	-----	-----
ehb2c.pk001.d17 (SEQ ID NO:7)	(842)	ACCTGGGAGATC-ATAAGGATATACTTAAATATA	-----	-----	-----
ehb2c.pk001.o18 (SEQ ID NO:9)	(860)	ATTGGGAGATGC-ATAAGGATATACTTAAATATA	-----	-----	-----
r10n.pk117.i23 (SEQ ID NO:13)	(719)	CAATTGACCA--AGCGAATCTGGCTAAGAAGCAGCTG	-----	-----	-----
rr1.pk005.h8 (SEQ ID NO:15)	(860)	CAATTGACCA--AGCGAATCTGGCTAAGAAGCAGCTGTA	-----	-----	-----
s11.pk0128.h7 (SEQ ID NO:17)	(948)	CAATTGACCA--AGCGAATCTGGCTAAGAAGCAGCTGTA	-----	-----	-----
vdb1c.pk001.k23 (SEQ ID NO:11)	(912)	CAATTGACCA--AGCGAATCTGGCTAAGAAGCAGCTGTA	-----	-----	-----
wdk5c.pk005.f22 (SEQ ID NO:19)	(768)	CAATTGACCA--AGCGAATCTGGCTAAGAAGCAGCTGTA	-----	-----	-----
M.lutupps (SEQ ID NO:23)	(735)	TTTTGGTGGCTT-ATA	-----	-----	-----
yeast rer2 (SEQ ID NO:25)	(836)	ATTGGAACCA-ATA GTTGAATTAA	-----	-----	-----
yeast srl1 (SEQ ID NO:27)	(951)	ATTGGAACCA-ATA CAGCTATGCTTTGTACAACCTTTCCAAACCC	-----	-----	-----
dms2c.pk005.c7 (SEQ ID NO:1)	(865)	-----	1101	1132	-----
ecs1c.pk009.p19 (SEQ ID NO:3)	(688)	-----	-----	-----	-----
ehb2c.pk001.i10 (SEQ ID NO:5)	(874)	-----	-----	-----	-----
ehb2c.pk001.d17 (SEQ ID NO:7)	(874)	-----	-----	-----	-----
ehb2c.pk001.o18 (SEQ ID NO:9)	(892)	-----	-----	-----	-----
r10n.pk117.i23 (SEQ ID NO:13)	(757)	-----	-----	-----	-----
rr1.pk005.h8 (SEQ ID NO:15)	(901)	-----	-----	-----	-----
s11.pk0128.h7 (SEQ ID NO:17)	(970)	-----	-----	-----	-----
vdb1c.pk001.k23 (SEQ ID NO:11)	(931)	-----	-----	-----	-----
wdk5c.pk005.f22 (SEQ ID NO:19)	(802)	-----	-----	-----	-----
M.lutupps (SEQ ID NO:23)	(751)	-----	-----	-----	-----
yeast rer2 (SEQ ID NO:25)	(862)	-----	-----	-----	-----
yeast srl1 (SEQ ID NO:27)	(1001)	CCATTTCAGTTTCGGTTACAGGAGATGAATAA	-----	-----	-----

FIG. 2-10

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1 50
 (1) --MLNLPYLPKP-----CYFPASLSTNHRGLYVF
 (1) -----
 (1) -----MELYNG
 (1) -----MELYNG
 (1) -----MEITYG
 (1) MLSEFPISADNARHTFSKSSCTFSNRIDSFSPPIVPRFKLRTA
 (1) -----
 (1) -----MLGSLMSYLPVSDSKTENTDEL
 (1) -----
 (1) MFSRLPIPLVKTPSPSCYYSHYYHYRYRCYHPFHRSQTQSLIVSK
 (1) -----MPLSN
 (1) -----

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

51 100
 (31) NQSDTTGGGINSLEERIT-----PAGKHHELPKHHVAVHMDGN
 (1) -----MPKHVAVHMDGN
 (7) ERPSFRLLGKMYMRKGLY-----STTQGPPIPTHIAHMDGN
 (7) ERPSFRLLEKMYMRKGLY-----STTQGPPIPTHIAHMDGN
 (7) QRPSPFRIFGKMYMRKGLY-----STTQGPPIPTHIAHMDGN
 (51) KTDVVGEEEAAREVNERAEFF-----PDGRRRELPETHVAVHMDGN
 (1) -----MPKHVAVHMDGN
 (23) IATGSLASLQNFIRKCI-----AVSYGPPKHHVAVHMDGN
 (51) RGSALAKCHADSVTLRDDGVSLAQESLEPLPAEPAEMVPHVAVHMDGN
 (6) STSSPAVTVPAAEELLS-----QGPAESLPRIHVALVMDGN

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

101 150
 (69) RRVARSECTMPDAGYMEARSKVMVELGRKWQIQLVAFSAADWLAP
 (13) RRIVVEKQWSPMTSHSMRKTQSLFROSKFKIAVSIKAFESTENWTRP
 (44) RRFAKHKHGGCHKAGFLALNVITVGVLEVMAIIVAFSIEDFRK
 (44) RRFAKHKHGGCHKAGFLALNVITVGVLEVMAIIVAFSIEDFRK
 (44) RRFAKHKHGGCHKAGFLALNVITVGVLEVMAIIVAFSIEDFRK
 (91) VRMAOKRGGGAASGHOAGVRSRELVELCKWGIIVLSVAFSYDWSAS
 (13) RRYAFFSIQGSGCHRVGFSALASLKGVMVMAIIVAFSIEDFRK
 (60) RRYAFFSIQGSGCHRVGFSALASLKGVMVMAIIVAFSIEDFRK

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)

FIG. 3-1

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s11.pk0128.h7 (SEQ ID NO:18) (101) GQVAVKQJPSACIQAGVQSLRKMVRLCSWGIIVLIVFAFESTENWVLP
 wdk5c.pk005.f22 (SEQ ID NO:20) (43) SQAARCTPTDCHHMRAMRTVRLSRAMGIRVLDAFGESLENNRP

dms2c.pk005.c7 (SEQ ID NO:2) (119) KVEDTGGIISVLKDEVVHMIKE---GIQLSVIYDTSKPKSKRIIT
 ecs1c.pk009.p19 (SEQ ID NO:4) (63) KEVDGEMEMYLRLRTDAEGLLSL---CRVSIMKKTNP3LOKLCI
 ehb2c.pk001.i10 (SEQ ID NO:6) (94) EHEVQYVDMLLEKEGMIMESIIINAYDICVRFVENIKLSEPVKTAD
 ehb2c.pk001.d17 (SEQ ID NO:8) (94) EHEVQYVDMLLEKEGMIMESIIINAYDICVRFVENIKLSEPVKTAD
 ehb2c.pk001.o18 (SEQ ID NO:10) (94) EREVQCVNMMKKEEELIIVESIMNAYDVGRIVENINLDEPIRIE
 rdb1c.pk001.k23 (SEQ ID NO:12) (141) EGVGTHSHIRVVVAELPILG---EKAFCRDWGFVKASEQLOLI
 r10n.pk117.i23 (SEQ ID NO:14) (63) ETVKSEMEVEEKNELLENRNVIKVNCKINFNENMDMISKSVRVAE
 rr1.pk0050.h8 (SEQ ID NO:16) (110) ETVKSEMEVEEKNELLENRNVIKVNCKINFNENMDMISKSVRVAE
 s11.pk0128.h7 (SEQ ID NO:18) (151) KVEDTGGIIRFRTINSEVQTFKRE---GIRISVIGDSSRIPESLKRMA
 wdk5c.pk005.f22 (SEQ ID NO:20) (93) KVEDTGGIIRFNDNLAEFLRE---GTRLRRIEDRSRPISSOKTAR

dms2c.pk005.c7 (SEQ ID NO:2) (166) YAENIKNSQINAVAINSGKYDLOQCOSIALKDKGVIQPEE---
 ecs1c.pk009.p19 (SEQ ID NO:4) (110) EIEEKSRAAGTHVNYLNISGKYDIEACKSVATKDGVIIPKQ---
 ehb2c.pk001.i10 (SEQ ID NO:6) (144) KIMRAVANNKCMILLIIVCTSDDEHHAVEESS--ELNSNEVCNN---
 ehb2c.pk001.d17 (SEQ ID NO:8) (144) KIMRAVANNKCMILLIIVCTSDDEHHAVEESS--ELNSNEVCNN---
 ehb2c.pk001.o18 (SEQ ID NO:10) (144) KIMRAVANNKCMILLIIVCTSDDEHHAVEESSKDKLNSNEVCNNGIEA
 vdb1c.pk001.k23 (SEQ ID NO:12) (186) DVEETKEKSRQFIWLSISGQCDLQCKNIGHKDKGLIEPD---
 r10n.pk117.i23 (SEQ ID NO:14) (113) KLMATIENTGTFSCMPNSISENNVNVKVC-----AER---
 rr1.pk0050.h8 (SEQ ID NO:16) (160) KLMATIENTGTFSCMPNSISENNVNVKVC-----AER---
 s11.pk0128.h7 (SEQ ID NO:18) (198) SAEEDKONSRFQIIVAGISGKYDVQCKSVAKKKGHIIHLDD---
 wdk5c.pk005.f22 (SEQ ID NO:20) (140) DAEATIRNSQIDVLIISIGRMDIYQACRNLAQWDAKLLRPED---

dms2c.pk005.c7 (SEQ ID NO:2) (212) -----INEFTIENIGINCIPFTHPDRT
 ecs1c.pk009.p19 (SEQ ID NO:4) (156) -----IDEKYFQOEGGKMDFYPDIVRT
 ehb2c.pk001.i10 (SEQ ID NO:6) (188) -QELEEANATGSSTVIQTENMESISGKIVDEKNNVIN--YPLVIRT
 ehb2c.pk001.d17 (SEQ ID NO:8) (188) -QELEEANATGSSTVIQTENMESISGKIVDEKNNVIN--YPLVIRT
 ehb2c.pk001.o18 (SEQ ID NO:10) (194) EQEFKEANGTG-NSVIPQKTESISGKIVDEKNNVIN--YPLVIRT
 vdb1c.pk001.k23 (SEQ ID NO:12) (232) -----INKSIEEQINCTEFTHPDRT
 r10n.pk117.i23 (SEQ ID NO:14) (150) ----R---DILQREDADSVANNNGVSDISVADDRHMVSAGCEDPDIVRT

FIG. 3-2

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rrl.pk0050.h8 (SEQ ID NO:16) ---R---DILQREDADSVANNGVSDISVADIDRHNVSAGCDPDIVIRI
 sl1.pk0128.h7 (SEQ ID NO:18) -----INENIEQDEENCTEFYDPDIIIRI
 wdk5c.pk005.f22 (SEQ ID NO:20) -----IDESIFADIIQI--SETSCPDIIRI

301 (238) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG 350
 (182) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (235) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (235) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (241) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (258) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (194) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (241) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (270) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG
 (210) SGLRVSNIFFLWOLAYTELISSETVETDIEDEELHNLNTQHRRRRYGG

351 (288) dms2c.pk005.c7 (SEQ ID NO:2) -----
 (229) ecs1c.pk009.p19 (SEQ ID NO:4) -----
 (285) ehb2c.pk001.i10 (SEQ ID NO:6) HKEYLA
 (285) ehb2c.pk001.d17 (SEQ ID NO:8) HKEYLA
 (291) ehb2c.pk001.o18 (SEQ ID NO:10) HKEYLA
 (308) vdb1c.pk001.k23 (SEQ ID NO:12) RN
 (244) r10n.pk117.i23 (SEQ ID NO:14) SRNLAKQL
 (291) rrl.pk0050.h8 (SEQ ID NO:16) SRNLAKQL
 (320) sl1.pk0128.h7 (SEQ ID NO:18) RHS
 (260) wdk5c.pk005.f22 (SEQ ID NO:20) RKNNAL--

FIG. 3-3

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1 50

M.lutUPPS (SEQ ID NO:24) -----

Yeaststr1 (SEQ ID NO:28) -----MKMPSIIQIQFVALKRLLVETKEQMCF

Yeastrer2 (SEQ ID NO:26) -----METDSGIP

dms2c.pk005.c7 (SEQ ID NO:2) -----CYFPASLSTNHHRGLYVF

ecs1c.pk009.p19 (SEQ ID NO:4) -----

ehb2c.pk001.i10 (SEQ ID NO:6) -----MELNG

ehb2c.pk001.d17 (SEQ ID NO:8) -----MELNG

ehb2c.pk001.o18 (SEQ ID NO:10) -----MEIYTG

vdb1c.pk001.k23 (SEQ ID NO:12) -----

r10n.pk117.i23 (SEQ ID NO:14) -----

rr1.pk0050.h8 (SEQ ID NO:16) -----MLGSLMSYLPVSDKTENTDEL

s11.pk0128.h7 (SEQ ID NO:18) -----MFSLRPLPLVKTPPSPCYSHYHYRYRCYHPFHRSQTQSLIVSK

wdk5c.pk005.f22 (SEQ ID NO:20) -----MPLSN

FIG. 4-1

51 100

M.lutUPPS (SEQ ID NO:24) -----

Yeaststr1 (SEQ ID NO:28) -----INAAQIKHIIHMDGN

Yeastrer2 (SEQ ID NO:26) -----AVKSIQFVFAWMSLSLFSWFYNLQNILIKARVGPVEHVSSEMDGN

dms2c.pk005.c7 (SEQ ID NO:2) -----GHSFQKWKTNIFSRTL-----ASNCVFRIMGEMMDGN

ecs1c.pk009.p19 (SEQ ID NO:4) -----NQSDTTGGGINSLEERIT-----PAGQKHELMKHAIVMDGN

ehb2c.pk001.i10 (SEQ ID NO:6) -----ERPSQFRLLGKYMKGKLY-----SIITQGPITTHIIVMDGN

ehb2c.pk001.d17 (SEQ ID NO:8) -----ERPSQFRLLGKYMKGKLY-----SIITQGPITTHIIVMDGN

ehb2c.pk001.o18 (SEQ ID NO:10) -----QRPSQFRIFGKYMKGKLY-----SIITQGPITTHIIVMDGN

vdb1c.pk001.k23 (SEQ ID NO:12) -----KTDVQGEAEAREVNERAEF-----PDGIRRELMEHIVMDGN

r10n.pk117.i23 (SEQ ID NO:14) -----IATGQLASLQNFIRKCI-----AVSYGPMKHIIVMDGN

rr1.pk0050.h8 (SEQ ID NO:16) -----RGSAIAKCHADSVTLRDDGVSQAQESLEPLPAEIAAEMMKHAIVMDGN

s11.pk0128.h7 (SEQ ID NO:18) -----STSSQPAVTVPAAEELLS-----QGIRAESLRAIVMDGN

wdk5c.pk005.f22 (SEQ ID NO:20) -----

101 150

M.lutUPPS (SEQ ID NO:24) -----

(32) GSWAKQKKMRIRIKGHEQMOTVKKITRYASDLQVRYLILVAESTENWSRP

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FIG. 4-2

Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rr1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

(78) RRYAASRRPVEVKKEGEGGLTLTYIKRLGVCVSAESENRRP
 (43) RRFARKKEMDVKEGEGFVMSRIIELEYAGVDTAVFAESENKRK
 (69) RRFARSRCMPDAGMEARSKVMVELRKWGIQVLFVESAEWLRP
 (13) RRFVEKGSWPMGSHMRKTQSLFRGSKFKIAVSIASETEWTRP
 (44) RRFARKHKEGEGGKFLALNVITYYELGVYAYIAESDENRRK
 (44) RRFARKHKEGEGGKFLALNVITYYELGVYAYIAESDENRRK
 (44) RRFARKHKEGEGGKFLALNVITYYELGVYAYIAESDENRRK
 (91) VFWAQRGCEHAASCHQVRSRELVELCKWGIKLSVFAFSYDWSRS
 (13) RRYAIFRSIOEGSCHRVFSAIASELYGEMGVYIIVNAESDENRRK
 (60) RRYAIFRSIOEGSCHRVFSAIASELYGEMGVYIIVNAESDENRRK
 (101) GRWAVKGVPSACQVQVSRKMVRLCSWGIIVLVFAESTENWVRP
 (43) SRWAAARGEPDCEHEMRALMRTVRLSRAGIIRVLDAFGSELENWVRP

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M.lutUPPS (SEQ ID NO:24)
 Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rr1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

(82) KDEVNYTKKPGDFLNTFLPELIEKN-----VKVETIGFIDDPDHTKKA
 (128) KEEDTNNFTVKLDEFKRAKDYKDPLYGSKIRIVEDQSISPENMRKK
 (93) SRVESMTARERPOITERGELACK--YGVRIKIIDLSIDKSLLED
 (119) KVEVDFMGIIISVLKDEVVHMIKE-----GIQLSVIDTSKPKGVKRI
 (63) KEVDFMEMYDILRTDAEELLSL-----GCRVSIMCKKTNPGLQKL
 (94) PHEVQYVMDMLEKEGMEEMESIINA--YDICRVFVGNLKLSEPVKTA
 (94) PHEVQYVMDMLEKEGMEEMESIINA--YDICRVFVGNLKLSEPVKTA
 (94) PREVQCVNMMKEEIIIEESIMNA--YDVGVRIVGNLNLDEPIRIA
 (141) EGVGFTVSIIRVVKAELPILG-----GKAFECRDWGFVKASEQLQL
 (63) PTEVKSMEEMKEENELLENRNVIN--VNCKINFWGNLDMSEVVRVA
 (110) PTEVKSMEEMKEENELLENRNVIN--VNCKINFWGNLDMSEVVRVA
 (151) KVEVDFMRFTNSENSEVQTFKRE-----GIRISVIDSSRPESLKRMM
 (93) KAEVDFMAIIRFINDNLAEFLRE-----GTLRIIDRSRPISVQKT

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M.lutUPPS (SEQ ID NO:24)
 Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)

(127) VLEAKKHKHTGLTAVFNLNGRKELISVQLIAERYKSGEISLDE--
 (178) IKKVEIIOGDGDFTFICFPYTSRNDMLHTIRDSVEDHLEN---KSP-
 (141) VRVAVTQKNKRAFNICFPYTEREHLHMKETIVQHKGAIDES--
 (164) IITYAENIKNNSQLNVVAINSGKYDVOQCOSIALKVKGQVIOPEE--
 (108) CIEIEKSRANSQTHVNYALNSGKYDIIECKSVATKVKGQVIOPEE--
 (142) ADKIMRANNSKCVLLIIVCTSTDEHVAHVEESS--ELNSNEVCNN--
 (142) ADKIMRANNSKCVLLIIVCTSTDEHVAHVEESS--ELNSNEVCNN--
 (142) AEKIMRANNSGFVLLIIVAVASSTDEHVAHVEESSKDKLNSNEVCNNGI

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FIG. 4-3

vdb1c.pk001.k23	(SEQ ID NO:12)	(184)	IIDVEITKENSRLQFIVALSISQCDILOACKNIGHKVKGDLIEPED--	300
r10n.pk117.i23	(SEQ ID NO:14)	(111)	AEKLNATAEINTGLVSVCMPIINSTSEANVNVKVC-----AER--	
rr1.pk0050.h8	(SEQ ID NO:16)	(158)	AEKLNATAEINTGLVSVCMPIINSTSEANVNVKVC-----AER--	
s11.pk0128.h7	(SEQ ID NO:18)	(196)	IASAEIDKONGRFQIVGVISGKYDVCKSVAKKVKDGHILDD--	
wdk5c.pk005.f22	(SEQ ID NO:20)	(138)	ARDAEAPARNVOLDVIVISGRMDVQACRNLAQKVDKLLRPED--	
M.lutUPPS	(SEQ ID NO:24)	(175)	-----ISETHFNEYLF--ANMDEEII	
Yeaststr1	(SEQ ID NO:28)	(223)	-----R-----NIRKFTNKMVG-FHSNKCEII	
Yeastrer2	(SEQ ID NO:26)	(189)	-----TLASHLYTAGVPLDII	
dms2c.pk005.c7	(SEQ ID NO:2)	(212)	-----INEFTIENLGNCIPPHDII	
ecs1c.pk009.p19	(SEQ ID NO:4)	(156)	-----DEKYFKQGLGKMKIDFVYDII	
ehb2c.pk001.i10	(SEQ ID NO:6)	(188)	---QELEEANATGSSTVIQTENMESYSIGIKLVLDKKNYIN--YEVVI	
ehb2c.pk001.d17	(SEQ ID NO:8)	(188)	---QELEEANATGSSTVIQTENMESYSIGIKLVLDKKNYIN--YEVVI	
ehb2c.pk001.o18	(SEQ ID NO:10)	(192)	EAEQEPKEANGTG-NSVIPQKTESYSGINLADLKKNYVNV--PHEDVI	
vdb1c.pk001.k23	(SEQ ID NO:12)	(232)	-----RKSLLIEQLQINCTEFEDII	
r10n.pk117.i23	(SEQ ID NO:14)	(150)	---R---DILQREDADSVANNGVYSDISVADLDRHMYSGCDDIIVI	
rr1.pk0050.h8	(SEQ ID NO:16)	(197)	---R---DILQREDADSVANNGVYSDISVADLDRHMYSGCDDIIVI	
s11.pk0128.h7	(SEQ ID NO:18)	(244)	-----NENIIEQLQINCTEFEDII	
wdk5c.pk005.f22	(SEQ ID NO:20)	(186)	-----IDESLIFADLQII--SETSCDII	
M.lutUPPS	(SEQ ID NO:24)	(197)	RTSGEIRSNFIMOCVSY--EFVIEIEFWIDNEESLAQCISIVQNRHR	350
Yeaststr1	(SEQ ID NO:28)	(247)	RTSGHRISDYIMOCVHEN-ATIESETTMEISFFAMYLMLKWSFFST	
Yeastrer2	(SEQ ID NO:26)	(207)	RTSGVSEISDIIIMOCVASSKGVRIELLQVPEEPIRMAWILLKESFHS	
dms2c.pk005.c7	(SEQ ID NO:2)	(236)	RTSGELVSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
ecs1c.pk009.p19	(SEQ ID NO:4)	(180)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
ehb2c.pk001.i10	(SEQ ID NO:6)	(233)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
ehb2c.pk001.d17	(SEQ ID NO:8)	(233)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
ehb2c.pk001.o18	(SEQ ID NO:10)	(239)	RTSGELVSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
vdb1c.pk001.k23	(SEQ ID NO:12)	(256)	RTSGELVSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
r10n.pk117.i23	(SEQ ID NO:14)	(192)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
rr1.pk0050.h8	(SEQ ID NO:16)	(239)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
s11.pk0128.h7	(SEQ ID NO:18)	(268)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	
wdk5c.pk005.f22	(SEQ ID NO:20)	(208)	RTSGEIRSNFIMOCVLAIT--EYVSETMDGEDELLHGLNTQHRRR	

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	351	RFGL	398
M.lutUPPS	(SEQ ID NO:24)	(245)	RFGL
Yeaststl	(SEQ ID NO:28)	(296)	IQYNEKNHSLFEKIHEVPSIFKFKKKTAMSLYNFPNPISVSTGDE
Yeastrer2	(SEQ ID NO:26)	(257)	FLNKEYRLEEGDYDEETNGDPIDLKEKLN
dms2c.pk005.c7	(SEQ ID NO:2)	(284)	RYGG
ecslc.pk009.p19	(SEQ ID NO:4)	(228)	C
ehb2c.pk001.i10	(SEQ ID NO:6)	(281)	YLEKHKEYLK
ehb2c.pk001.d17	(SEQ ID NO:8)	(281)	YLEKHKEYLK
ehb2c.pk001.o18	(SEQ ID NO:10)	(287)	YLEKHKEYLK
vdb1c.pk001.k23	(SEQ ID NO:12)	(304)	RYGGRN
r10n.pk117.i23	(SEQ ID NO:14)	(240)	SIEQSRNLAKKQL
rr1.pk0050.h8	(SEQ ID NO:16)	(287)	SIEQSRNLAKKQL
sl1.pk0128.h7	(SEQ ID NO:18)	(316)	RYGGRHS
wdk5c.pk005.f22	(SEQ ID NO:20)	(256)	RFGRKKNNAAL

FIG. 4-4

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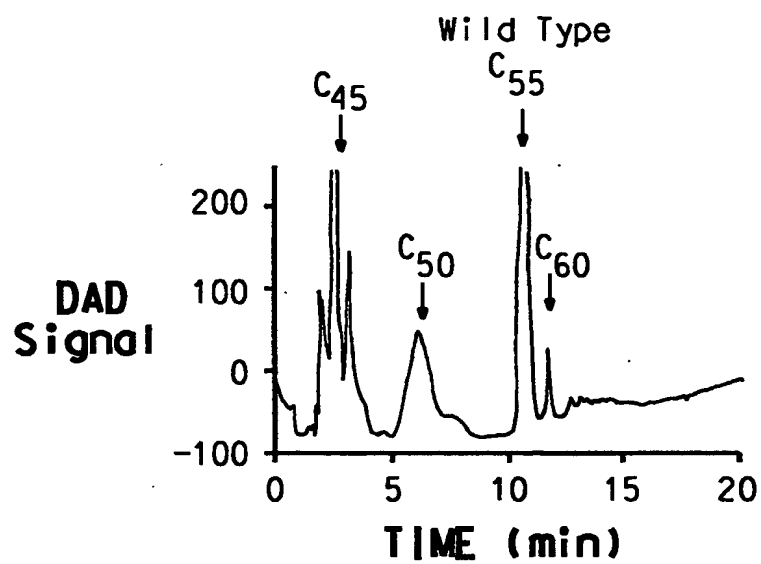


FIG. 5A

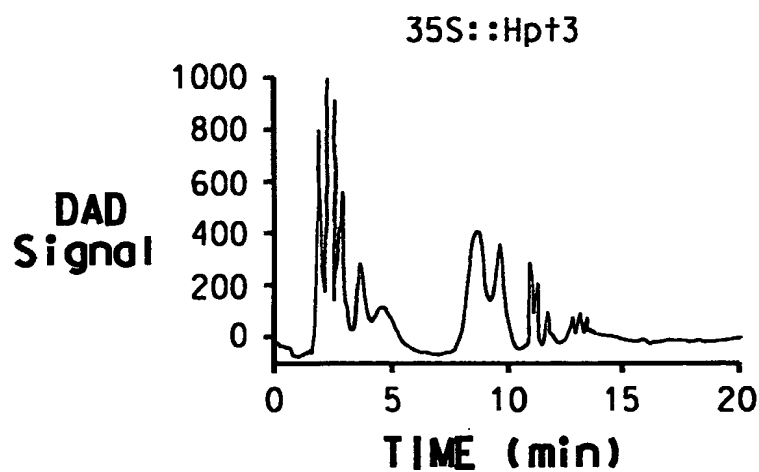


FIG. 5B

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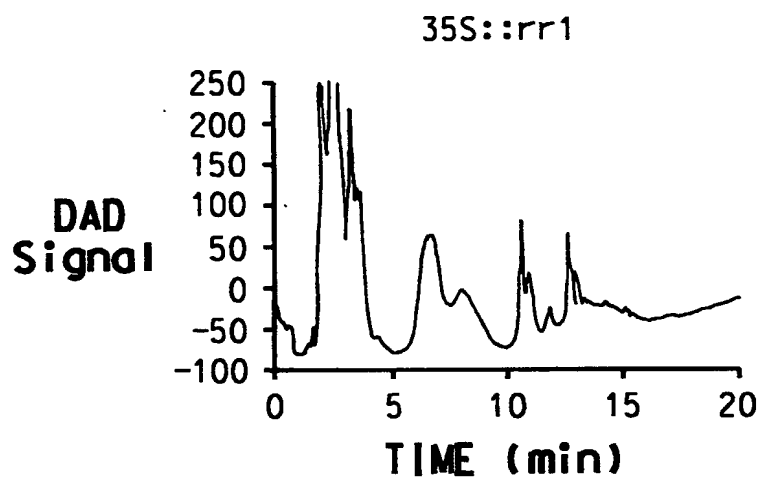


FIG. 5C

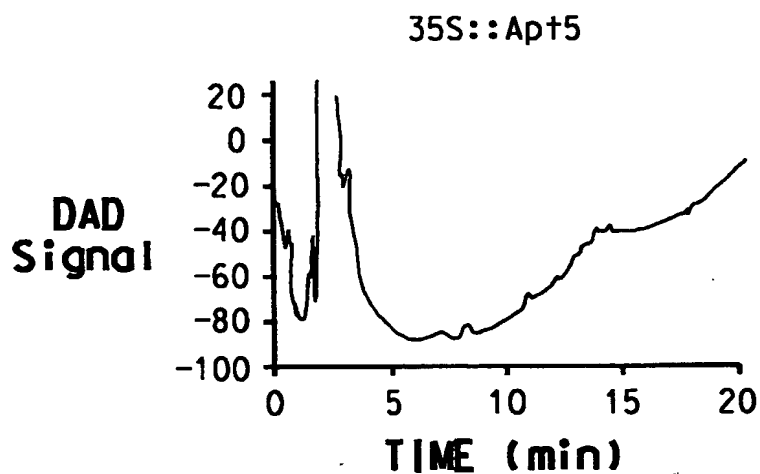


FIG. 5D

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35S::s11

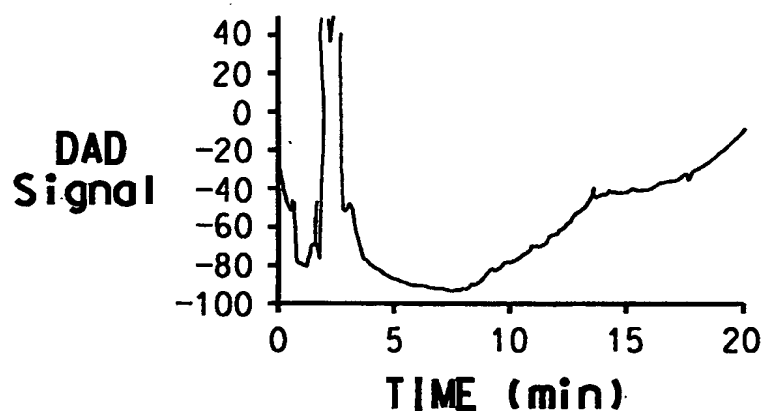


FIG. 5E

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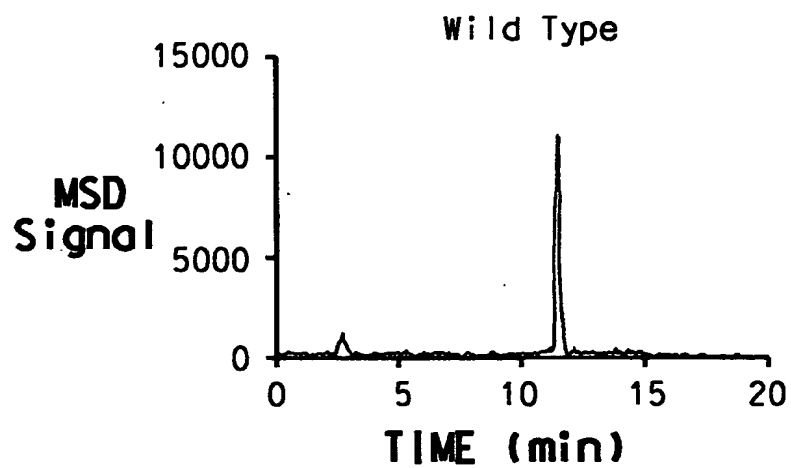


FIG. 6A

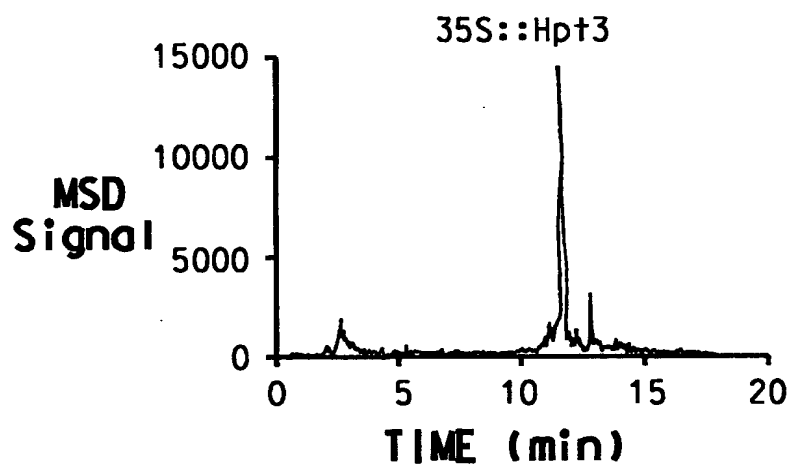


FIG. 6B

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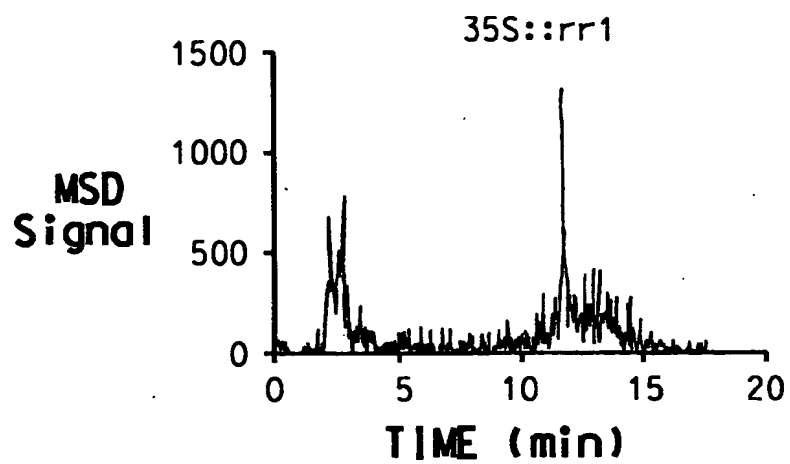


FIG. 6C

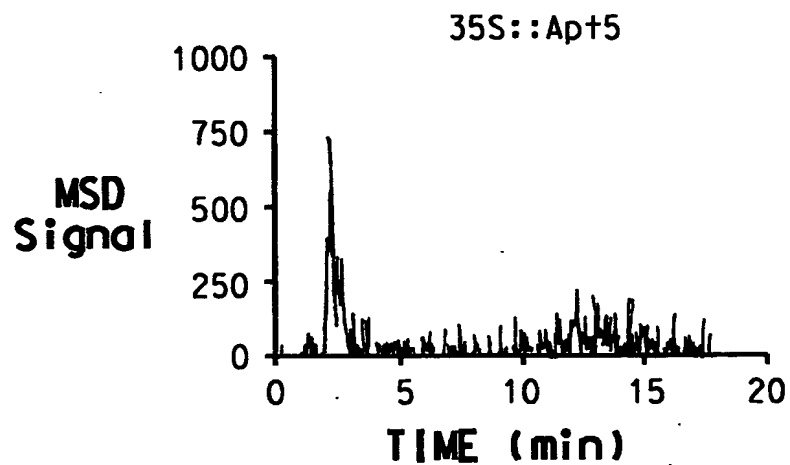


FIG. 6D

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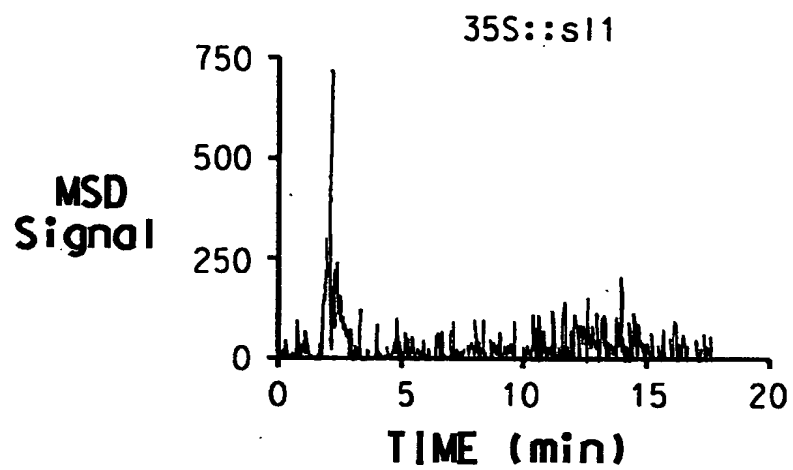


FIG. 6E

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> cis-Prenyltransferases from Plants

<130> BC1019 PCT

<140>

<141>

<150> 60/155,046

<151> 1999-09-21

<160> 37

<170> Microsoft Office 97

<210> 1

<211> 1388

<212> DNA

<213> Dimorphotheca

<400> 1

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gaattgtgag cggataacaa ttccacacag gaaacagcta tgaccatgat tacgccaagc 180
gcgcaattaa ccctcactaa agggaacaaa aggctggagc tccaccgcgg tggcgggccgc 240
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagcttaaa taatgcttaa 300
tcttcccctc tacttaacca aatatccttg ttatttcccg gcctctctct ccaccaacca 360
ccaccgtggt ctttatgtat tcaaccaatc agacaccact ggaggtggaa ttaattcgct 420
ggaggaacgc attactccag caggactcaa gcacgagtta atgccaaagc atgtggcagt 480
gatcatggat ggaaacagga gatgggctcg atcacgtggg ttaatgccgg atgctgggta 540
catggaaggt gcacgctcat tgaaggtgat ggtggaattg tgcgttaaat ggggaattca 600
agtccttact gtgtttgcct tctcagctga taactgggta agacccaaag ttgaagttga 660
tttcttgatg ggactaattg aaagtgtatt aaaagatgaa gttgttcata tgatcaaaga 720
gggtatccag ctttcgggta tcggagacac atctaagctt ccaaaatcgg taaaacggat 780
cattacatat gctgaaaaca tcacgaagaa caactcacia ctcaatcttg ttgtagcaat 840
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gagcaacttc tttttgtggc aattggcgta tactgaatta tacttcagtg aaactctttg 1080
gcctgatttt ggtgaagatg aacttttaca tgcttttaaat acttttcaac atagacgaag 1140
acgttatggt ggatgagatt cttaaacaac cctgtagagt tgcatatcat attgactttt 1200
gatatgtttc aatactattt atattattat tatgttgtaa taticgtacta gaacatgaat 1260
ttaaataggc aatagagcat gccaccta atgtctagtt atgagattct aaagacgtaa 1320
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<210> 2

<211> 287

<212> PRT

<213> Dimorphotheca

<400> 2

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Met Leu Asn Leu Pro Leu Tyr Leu Pro Lys Tyr Pro Cys Tyr Phe Pro
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Ala Ser Leu Ser Thr Asn His His Arg Gly Leu Tyr Val Phe Asn Gln
      20                      25                      30

Ser Asp Thr Thr Gly Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
 35                      40                      45

```

Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile
 50 55 60
 Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp
 65 70 75 80
 Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu
 85 90 95
 Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala
 100 105 110
 Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu
 115 120 125
 Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly
 130 135 140
 Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val
 145 150 155 160
 Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln
 165 170 175
 Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val
 180 185 190
 Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln
 195 200 205
 Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn
 210 215 220
 Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 225 230 235 240
 Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 245 250 255
 Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu
 260 265 270
 His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Arg Tyr Gly Gly
 275 280 285

<210> 3

<211> 1082

<212> DNA

<213> Calendula officinalis

<400> 3

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ttacaaatat atcaacggtt ttgagcaatg aaaataccaa actgaaaacc aaaaaagaa 180
gaagtagaat taccaggggg tctcgaagaa gaactaatgc caaaacacgt tgcattcata 240
atggatggaa accgtcgatg ggcgggtggaa aaaggttggt ctccaatgac ggggtcatagt 300
gccatgagaa agacgcttca atctctcctt tttcgaatgt ccaaattcaa aatcaaagcg 360
gtatcgattt atgcattttc taccgaaaat tggactcgcc cgaaggaaga agttgatttc 420
ctaattggaga tgtatgaaga tttattgagg acagatgctg aggagctctt aagtcttggt 480
tgtcgagtaa gcataatggg gaaaaagacc aaccttccga aatcactaca aaagttatgc 540
atcgaaatag aagaaaaatc aagagccaat tcaggaaccc atgttaacta tgcactcaac 600
tacagtggaa aatacgacat aatcgaagct tgtaaaagcg tcgctacaaa agtcaaggat 660

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ggtgttatta ttccaaaaca gatcgacgaa aaatatttca aacaagaact cggtagcaaaa 720
atgatcgatt ttccttaccc tgacctagtt atacgtacaa gcgggggaaat taggcttagt 780
aatttcacgc tatggcagat ggcgtatagc gagctttatt tcacggataa atactttccg 840
gattttgggg aaaatgatct tatcgaggct ttacttgcac ttcaaaaagt gcgtaaatgt 900
taataacttg ttgtgggtaa gacgagtgtg gtagaatatc aataaatgac tcgtttcggc 960
ggcgttgtgt atgccacatt atatgtctta gtgtctatca gaattcgaat ttgatttata 1020
gtcgttgtag atatgaaaac ttattatatt tgttcgatca aaaaaaaaaa aaaaaaaaaa 1080
aa 1082

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<210> 4

<211> 228

<212> PRT

<213> Calendula officinalis

<400> 4

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Met Pro Lys His Val Ala Phe Ile Met Asp Gly Asn Arg Arg Trp Ala
 1             5             10             15
Val Glu Lys Gly Trp Ser Pro Met Thr Gly His Ser Ala Met Arg Lys
          20             25             30
Thr Leu Gln Ser Leu Leu Phe Arg Cys Ser Lys Phe Lys Ile Lys Ala
          35             40             45
Val Ser Ile Tyr Ala Phe Ser Thr Glu Asn Trp Thr Arg Pro Lys Glu
          50             55             60
Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
 65             70             75             80
Ala Glu Glu Leu Leu Ser Leu Gly Cys Arg Val Ser Ile Met Gly Lys
          85             90             95
Lys Thr Asn Leu Pro Lys Ser Leu Gln Lys Leu Cys Ile Glu Ile Glu
          100            105            110
Glu Lys Ser Arg Ala Asn Ser Gly Thr His Val Asn Tyr Ala Leu Asn
          115            120            125
Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
          130            135            140
Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
          145            150            155            160
Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
          165            170            175
Leu Val Ile Arg Thr Ser Gly Glu Ile Arg Leu Ser Asn Phe Met Leu
          180            185            190
Trp Gln Met Ala Tyr Ser Glu Leu Tyr Phe Thr Asp Lys Tyr Phe Pro
          195            200            205
Asp Phe Gly Glu Asn Asp Leu Ile Glu Ala Leu Leu Ala Phe Gln Lys
          210            215            220
Val Arg Lys Cys
225

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<210> 5

<211> 1071

<212> DNA

<213> Hevea brasiliensis

<400> 5

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tacaggcttc gggttaaagc atcgtgatgt ggggtttaagg aaatggaatt atataccagt 120
taagtcagtg atttaaggaa aatggaatta tacaacgggtg agaggccaag tgtgttcaga 180
cttttaggga agtatatgag aaaaggggta tatagcatcc taaccagggtg tcccatccct 240
actcatattg ccttcatatt ggatggaaac aggaggtttg ctaagaagca taaactgcca 300
gaaggagggtg gtcataaggc tggattttta gctccttctga acgtactaac ttattgctat 360
gagttaggag tgaaatatgc gactatctat gccttttagca tcgataattt tcgaaggaaa 420
cctcatgagg ttcagtacgt aatggatcta atgctggaga agattgaagg gatgatcatg 480
gaagaaagta tcatcaatgc atatgatatt tgcgtacgtt ttgtgggtaa cctgaagcct 540
ttaagtgagc ccgtcaagac cgcagcagat aagattatga gggctactgc caacaattcc 600
aaatgtgtgc ttctcattgc tgtatgctat acttcaactg atgagatcgt gcatgctgtt 660
gaagaatcct ctgaattgaa ctccaatgaa gtttgtaaca atcaagaatt ggaggaggca 720
aatgcaactg gaagcagtac tgtgattcaa actgagaaca tggagtcgta ttctggaata 780
aaacttgtag accttgagaa aaacacctac ataaatcctt atcctgatgt tctgattcga 840
acttctgggg agacccgtct gagcaactac ttactttggc agactactaa ttgcatactg 900
tattctcctt atgcactgtg gccagagatt ggtcttcgac acgtggtgtg gtcagtaatt 960
aacttccaac gtcattattc ttacttggag aaacataagg aataactaaa ataatttggt 1020
tctgttccta gctcatcctg ccttattccg atagggttaag cttaagcata t 1071

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<210> 6

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 6

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Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Gly
  1           5           10          15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
      20           25          30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
      35           40          45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
      50           55          60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
      65           70          75          80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
      85           90          95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
      100          105          110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
      115          120          125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
      130          135          140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
      145          150          155          160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
      165          170          175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
      180          185          190

```

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285

Leu Lys
 290

<210> 7
 <211> 1000
 <212> DNA
 <213> Hevea brasiliensis

<400> 7
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 tcagactttt agagaagtat atgagaaaag gggttatatag catcctaacc cagggtccca 120
 tccctactca tattgccttc atattggatg gaaacaggag gtttgctaag aagcataaac 180
 tgccagaagg aggtgggtcat aaggctggat ttttagctct tctgaacgta ctaacttatt 240
 gctatgagtt aggagtgaat tatgcgacta tctatgcctt tagcatcgat aattttcgaa 300
 ggaaacctca tgaggttcag tacgtaatgg atctaattgct ggagaagatt gaagggatga 360
 tcatggaaga aagtatcatc aatgcatatg atatttgogt acgttttgtg ggtaacctga 420
 agctttttaag tgagccagtc aagaccgcag cagataagat tatgagggct actgccaaca 480
 attccaaatg tgtgcttctc attgctgtat gctatacttc aactgatgag atcgtgcatg 540
 ctgttgaaga atcctctgaa ttgaactcca atgaagtgtg taacaatcaa gaattggagg 600
 aggcaaatgc aactggaagc agtactgtga ttcaaactga gaacatggag tcgtattctg 660
 gaataaaaact tgtagacctt gagaaaaaca cctacataaa tccttatcct gatgttctga 720
 ttcgaacttc tggggagacc cgtctgagca actacttact ttggcagact actaattgca 780
 tactgtatct tccttatgca ctgtggccag agattgggtc tcgacacgtg gtgtgggtcag 840
 taattaactt ccaacgtcat tattcttact tggagaaaca taaggaatac ttaaaaataat 900
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<210> 8
 <211> 290
 <212> PRT
 <213> Hevea brasiliensis

<400> 8
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 1 5 10 15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
 20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
 50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
 65 70 75 80
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
 100 105 110
 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140
 Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
 145 150 155 160
 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190
 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285
 Leu Lys
 290

<210> 9

<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 9

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 aaggaaaatg gaaatatata cgggtcagag gccaaagtgtg tttagaattt ttgggaaata 120
 catgagaaaa ggggttatata gcatcctaac ccaagggtccc atccctactc atcttgctt 180
 cataatggat ggaaaccgga ggtttgctaa gaagcacaaa atgaaagaag cagaagggtta 240
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 gtatgtaacc atttatgcct ttagcattga taattttcga aggcaacctc gtgaggttca 360
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 gaatgcatat gatgttggcg tacgtattgt gggtaacctg aatcttttag atgagccaat 480
 caggatcgca gcagaaaaga ttatgagggc tactgccaat aattccgggt ttgtgcttct 540
 cattgctgta gcctatagtt caactgatga gatcgggcat gctgttgaag aatcctctaa 600
 agacaaattg aactccaatg aagtttgcaa caatgggatt gaagctgaac aggaatttaa 660
 ggaggcaaac ggaaccggaa acagtgtgat tccagttcag aagacggagt catattctgg 720
 aataaatctt gcagaccttg agaaaaacac ctacgtaaat cctcatcctg atgtcttgat 780

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tcgaacttct gggttgagcc gtctaagtaa ctacctactt tggcagacta gtaattgcat 840
actgtattct ccttttgacac tgtggccaga gattgggtctc aggcacttgg tatggacagt 900
aatgaacttc caacgtcatc attcttattt ggagaagcat aaggaatatt taaaataatt 960
tatttttgtt cctaactcat cctgccttat tcgggataga 1000

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<210> 10

<211> 296

<212> PRT

<213> Hevea brasiliensis

<400> 10

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Met Glu Ile Tyr Thr Gly Gln Arg Pro Ser Val Phe Arg Ile Phe Gly
  1             5             10             15
Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
          20             25             30
Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys
          35             40             45
Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala
          50             55             60
Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val
  65             70             75             80
Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
          85             90             95
Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
          100            105            110
Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val
          115            120            125
Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
  130            135            140
Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
  145            150            155            160
Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
          165            170            175
Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
          180            185            190
Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile
          195            200            205
Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu
  210            215            220
Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr
  225            230            235            240
Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn
          245            250            255
Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg
          260            265            270
His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu
          275            280            285

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Glu Lys His Lys Glu Tyr Leu Lys
290 295

<210> 11
<211> 1232
<212> DNA
<213> Vitis sp

<400> 11
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aatttcagct gataacgctc gccatacttt caagtccaaa cactcttctt gtacttttcc 120
aagtaacaga atcgattcat tttcttttcc tccaatctca gttcccagat ttcacaaact 180
tcgcacagct aaaactgatg tagttgggga agaagaagca agagaagtaa acgagagagc 240
ggaggaattt cgggacggtc ttcggagaga actgatgccg gaacacgtgg ccgtcattat 300
ggacgggaac gtgaggtggg cacagaagag ggggttgccg gcggcgtcgg gtcaccaagc 360
aggtgtgagg tcgttgagag agctgggtgga gctctgttgc aaatggggga tcaaagttct 420
ctcggttttc gcatttttct atgataattg gtctcgttcc gaaggggagg ttggttttct 480
tatgagcttg atcgaaagag tgggtcaaagc tgagctgcca attttgggag ggaaggcatt 540
cgagtgtcgt gattggggat ttgtcaaagc ttctgagcaa ctgcaactga taattgatgt 600
agaggagacc actaaggaga actcgcgatt acagttcatt gtggcactta gctatagtgg 660
gcagtgtgac atactacaag catgcaaaaa cattgggtcac aaagttaaagg atggccttat 720
cgaaccggaa gacatcaaca aaagccta at tgaacaggag ctacagacaa actgtactga 780
atttcccttc cctgatctac ttatacgaac tagtggcgaa cttagagtca gcaatttcat 840
gttgtggcaa atagcctaca ctgaactttg ctttttttagc acactgtggc ctgatttttg 900
gaaggatgag tttgtggagg ccttaagtgc ttttcagaaa aggagagac gatatggtgg 960
gcgaaactga gtttactaat tacatataga tccccaactt ctgctccatt catatggaga 1020
acttgtatac cattatatga agttaaatc ctgagaattc acttattaca cacagatccc 1080
caacctatac tccattcata tggaaaactt gtaccattat atgaaactca ttcttcagaa 1140
gggaactgat cataccctgc ttccaagtt taagcatgaa gtgccttgcc atttatatac 1200
atacttttac ttcaaaaaaa aaaaaaaa aa 1232

<210> 12
<211> 309
<212> PRT
<213> Vitis sp

<400> 12
Met Leu Ser Phe Arg Phe Pro Ile Ser Ala Asp Asn Ala Arg His Thr
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Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
50 55 60
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
 130 135 140
 Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
 145 150 155 160
 Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
 165 170 175
 Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
 180 185 190
 Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
 195 200 205
 Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
 210 215 220
 Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
 225 230 235 240
 Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
 245 250 255
 Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
 260 265 270
 Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
 275 280 285
 Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
 290 295 300
 Tyr Gly Gly Arg Asn
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<210> 13
 <211> 1021
 <212> DNA
 <213> Oryza sativa

<400> 13
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 ggctctgggc acaggggtggg cttctctgct ctcattgcca gcctgctcta ctgctatgaa 180
 atgggcgtga agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240
 actgaggtga aatccttgat ggagttaatg gaggaaga tcaatgaact gctagaaaac 300
 agaaatgtca tcaacaagggt taactgtaag atcaacttct gggggaactt ggacatgttg 360
 agcaaatcag tgagggtagc agctgagaaa ctgatggcta ccactgctga aaacacggga 420
 ctggtcttct ctgtttgcat gccatacaac tccacttctg agattgtcaa tgcggtcaat 480
 aaggctctgtg cagaaaggag ggatatactg cagaggaggag atgctgacag tgttgcaaat 540
 aatggtgtgt attcagacat ttcagtggca gatctggacc gccatatgta cagcgtggt 600
 tgccccgac ctgacattgt gatccggacc tcaggtgaga ctgcctgag caatttcctt 660
 ctgtggcaga cgacgttcag tcatttgcag aatccagacc ctctttggcc ggagttctct 720
 ttcaagcacc ttgtctgggc catactccag taccaaagag ttcacccttc tattgagcaa 780
 agcagaaatc tggctaagaa gcagctgtaa tcacatcctc cctgggagga gatagaaacc 840
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 tatgaaatat ataaaggata gctatgccat tgtatgcttg aacatgtgta tgcctgagtt 960
 ggtccaaatg tgtgaaatgt aataacattt ggtctaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 a 1021

<210> 14
 <211> 252
 <212> PRT
 <213> Oryza sativa

<400> 14
 Met Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala
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 Lys Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser
 20 25 30
 Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr
 35 40 45
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
 50 55 60
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
 65 70 75 80
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
 85 90 95
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
 100 105 110
 Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
 115 120 125
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
 130 135 140
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
 145 150 155 160
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
 165 170 175
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
 180 185 190
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
 195 200 205
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
 210 215 220
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
 225 230 235 240
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 245 250

<210> 15
 <211> 900
 <212> DNA
 <213> Oryza sativa

<400> 15
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 gagttaattg cgactggtgt tcttgctagt ctgcagaatt tcatccgcaa atgcattgta 120
 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180


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agatatgcta aattcaggag tatccaggaa ggctctgggc acaggggtggg cttctctgct 240
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tttagcatcg ataattttaa gcgagatccg actgagggtga aatccttgat ggagttaatg 360
gaggaaaaga tcaatgaact gctagaaaac agaaatgtca tcaacaagggt taactgtaag 420
atcaacttct gggggaactt ggacatgttg agcaaatcag tgagggttagc agctgagaaa 480
ctgatggcta cactgctga aaacacggga ctggtcttct ctgtttgcat gccatacaac 540
tccacttctg agattgtcaa tgcggtcaat aagggtctgtg cagaaaggag ggatatactg 600
cagagggagg atgctgacag tgttgcaat aatggtgtgt attcagacat ttcagtggca 660
gatctggacc gccatatgta cagcgctggg tgccccgac ctgacattgt gatccggacc 720
tcaggtgaga ctcgctgag caatttcctt ctgtggcaga cgacgttcag tcatttgtag 780
aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840
taccaaagag ttcacccttc tattgagcaa agcagaaatc tggctaagaa gcagctgtaa 900

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<210> 16

<211> 299

<212> PRT

<213> *Oryza sativa*

<400> 16

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Met Leu Gly Ser Leu Met Ser Tyr Leu Pro Ser Val Asp Ser Lys Thr
  1             5             10             15

```

```

Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
      20             25             30

```

```

Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
      35             40             45

```

```

Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
      50             55             60

```

```

Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
      65             70             75             80

```

```

Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
      85             90             95

```

```

Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
      100            105            110

```

```

Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
      115            120            125

```

```

Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
      130            135            140

```

```

Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
      145            150            155            160

```

```

Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
      165            170            175

```

```

Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
      180            185            190

```

```

Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
      195            200            205

```

```

Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
      210            215            220

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```

His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
      225            230            235            240

```

Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe
 245 250 255

Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys
 260 265 270

His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile
 275 280 285

Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 290 295

<210> 17
 <211> 1028
 <212> DNA
 <213> Glycine max

<400> 17
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 attctcacta ttatcactat cgttatcggt atcgttggtta tcatcctttc catcaccggt 180
 cccaaacaca gagtcttatt gtctcgaagc gcggttccgc cattgcgaag tgtcacgctg 240
 atagcgtgac acttcgtgat gacggagtct cgctcgccca agagtcggtg gagccacttc 300
 cggcggaact cgcggcggag atgatgccga agcatgtggc ggtgataatg gacgggaacg 360
 ggaggtgggc gaaggtgaag gggctgccac catcggcggg gcaccaggcg ggggtgcaat 420
 cgctgaggaa aatggtgagg ctgtgttgca gctggggaat taaggttcta acggttttcg 480
 cgttctctac ggataactgg gttcgccccca aggtggaggt tgatttcttg atgaggctgt 540
 ttgagagAAC aataaaactct gaagttcaaa cttttaagag ggaaggaatt agaatatctg 600
 tgattggaga ttcatcaagg ttgcctgagt ctttaaaaag aatgatagct agtgcagaag 660
 aggatacaaa acaaaaattcg agattccaac ttattgtggc agtgggatac agtggaaaat 720
 atgatgttgt gcaagcatgt aaaaagtgtag ccaagaaaag caaagatggt cacattcact 780
 tggatgacat aaacgaaaac attattgaac aagaattgga aactaattgt actgagtttc 840
 cttatcctga tctactaata cgaactagtg gcgagcttag agtgagtaac ttcttggtgt 900
 ggcaattagc ctacacagaa ctttatttta atcgggaact ctggccagat tttgggaagg 960
 atgagtttgt agatgcatta agttcatttc aacaaagaca aagacgctat ggtggtcgac 1020
 attcataa 1028

<210> 18
 <211> 322
 <212> PRT
 <213> Glycine max

<400> 18
 Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
 1 5 10 15

Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
 20 25 30

Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
 35 40 45

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
 50 55 60

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
 65 70 75 80

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
 85 90 95

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
100 105 110

Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
115 120 125

Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
130 135 140

Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
145 150 155 160

Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
165 170 175

Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg
305 310 315 320

His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gggaactcgc	ggtgggcggc	agcgcggggc	ctgccgccga	cggacgggca	cgagcacggg	180
atgcgcgcgc	tgatgaggac	ggtgcggctc	tcccgcgcct	ggggcatccg	cgtcctcacc	240
gccttcgggt	tctcgctcga	gaactggaat	cgccccaaag	cggaggttga	cttcttgatg	300
gccttgatcg	agaggtttat	caacgacaac	ctcgccgagt	tcttgaggga	agggaccctg	360
ctacgtataa	tcggtgaccg	ctcaaggctg	ccgatctctg	tcgagaagac	tcgacgagac	420
gccgaggagg	caacaagaaa	caactcgcat	ctcgatctag	tcctagccat	cagctacagc	480
gggcgaatgg	acattgtgca	ggcatgccgg	aatctcgccc	agaaagtggg	cgccaagctg	540
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tcttgcccgg	acctgctcat	caggaccagc	ggcgagctga	ggctgagcaa	cttcctgcta	660
tggcagtcgg	cttactcgga	gctcttcttc	accgacacgc	tctggcctga	tttcggggag	720
gccaatatc	tccaagccat	gatggccttc	cacagcagag	acaggcgctt	tggaagaaga	780
aaaaacaatg	cagcgclata	aataaacggt	gcacgcgcgt	gacccgatgc	tcgatcatcc	840

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tctatctatc tgtatctgcc ttataaatca gtttttatta ccttcaaata aagtgtttct 900
ctcaagatgc gtgggtgtact ataggagagg ctactaaaac ttctctccag tgatttttact 960
ctatgctata tgctcattgt atttgatata gtttagcatt catgccgaaa aaaaaaaaaa 1020
aaaaaa 1026

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<210> 20

<211> 266

<212> PRT

<213> *Triticum aestivum*

<400> 20

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Met Pro Leu Ser Asn Ser Thr Ser Ser Val Pro Ala Val Thr Val Pro
1 5 10 15

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Ala Ala Glu Glu Leu Leu Ser Gln Gly Leu Arg Ala Glu Ser Leu Pro
20 25 30

```

```

Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
35 40 45

```

```

Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
50 55 60

```

```

Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
65 70 75 80

```

```

Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
85 90 95

```

```

Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
100 105 110

```

```

Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
115 120 125

```

```

Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
130 135 140

```

```

Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
145 150 155 160

```

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Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
165 170 175

```

```

Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
180 185 190

```

```

Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
195 200 205

```

```

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
210 215 220

```

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Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
225 230 235 240

```

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Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
245 250 255

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Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
260 265

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<210> 21

<211> 11

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Domain I of
 published alignment

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 <221> UNSURE
 <222> (2)..(3)
 <223> X = any amino acid

 <220>
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 <222> (8)
 <223> X = any amino acid

 <220>
 <221> UNSURE
 <222> (10)
 <223> X = any amino acid

 <300>
 <301> Apfel, C. M.
 <302> Use of Genomincs to Indentify Bacterial Undecaprenyl
 Pyrophosphate Synthetase: Clooning, Expression, and
 Characterization of the Essential uppS Gene
 <303> J. Bacteriol.
 <304> 81
 <306> 483-492
 <307> 1999

 <400> 21
 His Xaa Xaa Met Asp Gly Asn Xaa Arg Xaa Ala
 1 5 10

 <210> 22
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Domain V of published
 alignment

 <220>
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 <222> (3)
 <223> X = any amino acid

 <220>
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 <222> (7)
 <223> X = any amino acid

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 <223> X = any amino acid

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 <222> (12)
 <223> X = any amino acid

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 <223> X = any amino acid

<400> 22
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 Leu Trp Gln Xaa Xaa Tyr Xaa Glu
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<210> 23
 <211> 750
 <212> DNA
 <213> Micrococcus luteus

<300>
 <301> Shimizu, N.
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl
 Diphosphate Synthase: No Sequence Similarity between E- and
 Z-prenyl Diphosphate Synthases
 <303> J. Biol. Chem.
 <304> 273
 <306> 19476-19481
 <307> 1998

<400> 23
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 aatgaatatt tatttacagc aaatatgcct gatcctgagt tgtaaatcag aacttccggt 600
 gaagaacggt taagtaactt tttaatttgg caatgttcat atagtgagtt tgtatttata 660
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 aatcgtcacg gacgtttttg tggattataa 750

<210> 24
 <211> 249
 <212> PRT
 <213> Micrococcus luteus

<400> 24
 Met Phe Pro Ile Lys Lys Arg Lys Ala Ile Lys Asn Asn Asn Ile Asn
 1 5 10 15
 Ala Ala Gln Ile Pro Lys His Ile Ala Ile Ile Met Asp Gly Asn Gly
 20 25 30
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
 35 40 45
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
 50 55 60
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg
 65 70 75 80

Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu
85 90 95

Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr
100 105 110

Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu
115 120 125

Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe
130 135 140

Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu
145 150 155 160

Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser
165 170 175

Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro
180 185 190

Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu
195 200 205

Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp
210 215 220

Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln
225 230 235 240

Asn Arg His Arg Arg Phe Gly Gly Leu
245

<210> 25

<211> 861

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<308> AB013497

<400> 25

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gggaacagga gattcgctag aaagaaagag atggacgtaa aggaggcca cgaggcagga 180
tttgtagta tgagtagaat cttagaactg tggtatgaag caggagtcga tacggctacc 240
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aagggcgccg ctatagacga aagcacgtta gaatcgcatc tctacacggc gggggtaccc 600
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cctatacggg tggcatggat tttattaaaa ttttcgtttc acaaatcctt tttaaacaaa 780
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<210> 26

<211> 286

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

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 20 25 30
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
 35 40 45
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
 50 55 60
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
 65 70 75 80
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
 85 90 95
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
 100 105 110
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
 115 120 125
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
 130 135 140
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
 145 150 155 160
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
 165 170 175
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270
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Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp
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Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly
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Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr
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Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly
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Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys
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Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys
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Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu
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Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys
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Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys
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Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr
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Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr
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Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
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 Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu
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